



H8

SEQUENCE LISTING

<110> Arkowitz, Robert A
Nern, Peter MA

<120> NUCLEOTIDE SEQUENCES AND PROTEIN SEQUENCES

<130> DY0U13.1A2CP1

<140> 10/054399

<141> 2002-01-21

<150> 09/168,474

<151> 1998-10-08

<150> 08/951,141

<151> 1997-10-15

<150> 09/529,106

<151> 2000-04-07

<150> US 09/732,180

<151> 2000-12-07

<150> US 60/169,699

<151> 1999-12-07

<150> PCT/GB98/03033

<151> 1998-10-08

<150> 9812793.9

<151> 1998-06-12

<150> 9721357.3

<151> 1997-10-08

<150> 9721358.1

<151> 1997-10-08

<160> 37

<170> PatentIn Ver. 2.0

<210> 1

<211> 228

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<223>

<400> 1

```
ccccctctgta tactttttcaa ctctgtgaag ccgcaattta aattaccggt aatagcatct 60
gacgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaacac 120
tttgcattha acgatgagga gcttttctact atatccgacg tttttgccaa ctgcacgtcc 180
cagctggtca aagtgtctaga agtagtagaa acgctaata attccagc 228
```

<210> 2

<211> 76

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223>

<400> 2

Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15

Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 3

<211> 228

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid

<400> 3

ccctctgtgta tacttttcaa ctctgtgaag ccgcaattta aattaccggt aatagcattt 60
gacgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaacac 120
tttgattta acgatgagga gcttttcact atatccgacg tttttgcca ctcgacgtcc 180
cagctgggtca aagtgtctaga agtagtagaa acgctaata attccagc 228

<210> 4

<211> 76

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid

<400> 4

Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15

Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30

Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45

Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60

Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 5

<211> 228

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid

<400> 5
cccctctgta tactttttcaa ctctgtgaag ccgcaattta aattaccggt aatagcatct 60
ggcgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaacac 120
tttgatttta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctgggtca aagtgctaga agtagtagaa acgctaata attccagc 228

<210> 6
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

<400> 6
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
1 5 10 15
Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
20 25 30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
35 40 45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
50 55 60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser
65 70 75

<210> 7
<211> 228
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: nucleic acid

<400> 7
cccctctgta tactttttcaa ctctgtgaag ccgcaattta aattaccggt aatagcacct 60
gacgatttga aagtctgtaa aaaatccatt tatgacttta tattgggctg caagaaacac 120
tttgatttta acgatgagga gcttttcact atatccgacg tttttgccaa ctcgacgtcc 180
cagctgggtca aagtgctaga agtagtagaa acgctaata attccagc 228

<210> 8
<211> 76
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid

<400> 8
Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro

1	5	10	15
Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp	20	25	30
Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu	35	40	45
Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys	50	55	60
Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser	65	70	75

<210> 9
 <211> 392
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: amino acid

<400> 9
Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp
1 5 10 15
Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu
20 25 30
Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala
35 40 45
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu
50 55 60
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys
65 70 75 80
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala
85 90 95
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser
100 105 110
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr
115 120 125
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu
130 135 140
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala
145 150 155 160
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg
165 170 175
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val
180 185 190
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe

<400> 10						
atggcacatc	agatggactc	gataacgtat	tctaataatg	tcacccaaca	gtatatacaa	60
ccacaaagtc	tacaggatat	ctctgcagtg	gaggaagaaa	ttcaaaaataa	aatagagggc	120
gccagacaag	agagtaatac	gcttcatgtg	caaataaata	aagcaaaaaca	caagatacaa	180
gatgcaagct	tattccagat	ggccaacaaa	gttacttcgt	tgacaaaaaa	taagatcaac	240
ttaaagccaa	atatcgtgtt	gaaaggccat	aataataaaa	tctcagattt	tcggtggagt	300
cgagattcaa	aacgtatttt	gagtgcgaag	caagatggct	ttatgcttat	atggggacagt	360
gcttcagggt	taaaacagaa	cgctattcca	ttagattctc	aatgggttct	ttcctcgctt	420
atttcgccat	cgagtacttt	ggtagcaagc	cgaggattaa	acaataactg	taccatttat	480
agagtttcga	aagaaaacag	agtagcgcaa	aacgttgcgt	caattttcaa	aggacatact	540
tgctatatatt	ctgacattga	atttacagat	aacgcacata	tattgacagc	aagtggggat	600
atgacatgtg	ccttgtggga	tataccgaaa	gcaaagaggg	tgagagaata	ttctgaccat	660
ttaggtgatg	ttttggcatt	agctattcct	gaagagccaa	acttagaaaa	ttcttcgaac	720
acattcgcta	gctgtggatc	agacgggtat	acttacatat	gggatagcaq	atctccgtcc	780

gctgtacaaa gcttttacgt taacgatagt gatattaatg cacttcgttt ttccaagac 840
 gggatgtcga ttgttgcagg aagtgacaat ggtgcgataa atatgtatga ttaagggtcg 900
 gactgttcta ttgtacttt ttctcttttt cgaggttatg aagaacgtac ccctacccct 960
 acttatatgg cagctaacat ggagtacaat accgcgcaat cgccacaaac tttaaaatca 1020
 acaagctcaa gctatctaga caaccaaggc gttgtttctt tagatttttag tgcattctgga 1080
 agattgatgt actcatgcta tacagacatt ggttgtgttg tgtgggatgt attaaaagga 1140
 gagattgttg gaaaattaga aggtcatggt ggcagagtca ctggtgtgcg ctcgagtcca 1200
 gatgggtag ctgtatgtac aggttcatgg gactcaacca tgaaaatatg gtctccaggt 1260
 tatcaatag 1269

<210> 11
 <211> 422
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<220>
 <223>

<400> 11
 Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
 1 5 10 15
 Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
 20 25 30
 Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
 35 40 45
 His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
 50 55 60
 Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
 65 70 75 80
 Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
 85 90 95
 Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
 100 105 110
 Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
 115 120 125
 Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
 130 135 140
 Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
 145 150 155 160
 Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
 165 170 175
 Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
 180 185 190
 His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
 195 200 205
 Pro Lys Ala Lys Arg Val Arg Glu Tyr Ser Asp His Leu Gly Asp Val
 210 215 220

Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn
 225 230 235 240
 Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser
 245 250 255
 Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile
 260 265 270
 Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser
 275 280 285
 Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile
 290 295 300
 Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro
 305 310 315 320
 Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln
 325 330 335
 Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val
 340 345 350
 Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr
 355 360 365
 Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly
 370 375 380
 Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro
 385 390 395 400
 Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile
 405 410 415
 Trp Ser Pro Gly Tyr Gln
 420

<210> 12

<211> 1269

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: nucleic acid

<400> 12

atggcacatc agatggactc gataacgtat tctaataatg tcaccaaca gtatatataa 60
 ccacaaagtc tacaggatat ctctgcagtg gaggaagaaa ttcaaaataa aatagaggcc 120
 gccagacaag agagtaaaca gcttcagtct caaataaata aagcaaaaca caagatacaa 180
 gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
 ttaaagccaa atatcgtgtt gaaaggccat aataataaaa tctcagattt tccgtggagt 300
 cgagattcaa aacgtatttt gagtgcaggt caagatggct ttatgcttat atgggacagt 360
 gcttcagggt taaaacagaa cgctattcca ttagattctc aatgggttct ttctgcgct 420
 atttcgccat cgagtacttt ggtagcaagc gcaggattaa acaataactg taccatttat 480
 agagtttcga aagaaaacag agtagcgcaa aacgttgctt caattttcaa aggacatact 540
 tgctatattt ctgacattga atttacagat aacgcacata tattgacagc aagtggggat 600
 atgacatgtg ccttgtggga tataaccgaa gcaaagaggg tgagaggata ttctgacct 660
 ttaggtgatg ttttggcatt agctattcct gaagagccaa acttagaaaa ttcttcgaac 720

acattcgcta gctgtggatc agacgggtat acttacatat gggatagcag atctccgtcc 780
gctgtacaaa gctttttacgt taacgatagt gatattaatg cacttcgttt tttcaaagac 840
gggatgtcga ttgttgcagg aagtgacaat ggtgcgataa atatgtatga ttttaaggctcg 900
gactgttcta ttgtactttt ttctcttttt cgaggttatg aagaacgtac ccctaccct 960
acttatatgg cagctaacat ggagtacaat accgcgcaat cgccacaaac tttaaaatca 1020
acaagctcaa gctatctaga caaccaaggc gttgttttctt tagatttttag tgcattctgga 1080
agattgatgt actcatgcta tacagacatt ggttgtgttg tgtgggatgt attaaaagga 1140
gagattgttg gaaaattaga aggtcatggt ggcagagtca ctggtgtgcg ctcgagtcca 1200
gatgggtag ctgtatgtac aggttcattg gactcaacca tgaaaatatg gtctccaggt 1260
tatcaatag 1269

<210> 13

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amino acid
sequence

<400> 13

Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
1 5 10 15

Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
20 25 30

Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
35 40 45

His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
50 55 60

Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
65 70 75 80

Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
85 90 95

Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
100 105 110

Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
115 120 125

Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
130 135 140

Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
145 150 155 160

Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
165 170 175

Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
180 185 190

His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile
195 200 205

Pro Lys Ala Lys Arg Val Arg Gly Tyr Ser Asp His Leu Gly Asp Val

210	215	220
Leu Ala Leu Ala Ile	Pro Glu Glu Pro Asn	Leu Glu Asn Ser Ser Asn
225	230	235 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser		
	245	250 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile		
	260	265 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser		
	275	280 285
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile		
	290	295 300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro		
305	310	315 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln		
	325	330 335
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Val Val		
	340	345 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr		
	355	360 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly		
	370	375 380
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro		
385	390	395 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile		
	405	410 415
Trp Ser Pro Gly Tyr Gln		
	420	

<210> 14
 <211> 1269
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: nucleic acid
 sequence

<400> 14
 atggcacatc agatggactc gataacgtat tctaataatg tcacccaaca gtatatacaa 60
 ccacaaagtc tacaggatat ctctgcagtg gaggaagaaa ttcaaaataa aatagaggcc 120
 gccagacaag agagtaaaca gcttcatgct caaataaata aagcaaaaca caagatacaa 180
 gatgcaagct tattccagat ggccaacaaa gttacttcgt tgaccaaaaa taagatcaac 240
 ttaaagccaa atatcgtgtt gaaaggccat aataataaaa tctcagattt tcggtggagt 300
 cgagattcaa aacgtatttt gagtgcaggt caagatggct ttatgcttat atgggacagt 360
 gcttcagggt taaaacagaa cgctattcca ttagattctc aatgggttct ttctgcgct 420
 atttcgccat cgagtacttt ggtagcaagc gcaggattaa acaataactg taccatttat 480
 agagtttcga aagaaaacag agtagcgcaa aacgttgcgt caattttcaa aggacatact 540

tgctatatatt ctgacattga atttacagat aacgcacata tattgacagc aagtggggat 600
 atgacatgtg ccttgtggga tataccgaaa gcaaagaggg tgagagaata ttctgaccat 660
 ttaggtgatg ttttggcatt agctattcct gaagagccaa acttagaaaa ttcttcgaac 720
 acattcgcta gctgtggatc agacgggtat acttacatat gggatagcag atctccgtcc 780
 gctgtacaaa gcttttacgt taacgatagt gatattaatg cacttcggtt tttcaaagac 840
 gggatgtcga ttgttgcagg aagtgacaat ggtgcgataa atatgtatga ttttaaggctg 900
 gactgttcta ttgtactttt ttctcttttt cgaggttatg aagaacgtac ccctaccctc 960
 acttatatgg cagctaacat ggagtacaat accgcgcaat cgccacaaac tttaaaatca 1020
 acaagctcaa gctatctaga caaccaaggg gctgtttctt tagatttttag tgcattctgga 1080
 agattgatgt actcatgcta tacagacatt ggttgtgttg tgtgggatgt attaaaagga 1140
 gagattgttg gaaaattaga aggtcatggt ggcagagtca ctggtgtgcg ctcgagtcga 1200
 gatgggttag ctgtatgtac aggttcattg gactcaacca tgaaaatatg gtctccagg 1260
 tatcaatag 1269

<210> 15
 <211> 422
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: amino acid
 sequence

<400> 15
 Met Ala His Gln Met Asp Ser Ile Thr Tyr Ser Asn Asn Val Thr Gln
 1 5 10 15
 Gln Tyr Ile Gln Pro Gln Ser Leu Gln Asp Ile Ser Ala Val Glu Glu
 20 25 30
 Glu Ile Gln Asn Lys Ile Glu Ala Ala Arg Gln Glu Ser Lys Gln Leu
 35 40 45
 His Ala Gln Ile Asn Lys Ala Lys His Lys Ile Gln Asp Ala Ser Leu
 50 55 60
 Phe Gln Met Ala Asn Lys Val Thr Ser Leu Thr Lys Asn Lys Ile Asn
 65 70 75 80
 Leu Lys Pro Asn Ile Val Leu Lys Gly His Asn Asn Lys Ile Ser Asp
 85 90 95
 Phe Arg Trp Ser Arg Asp Ser Lys Arg Ile Leu Ser Ala Ser Gln Asp
 100 105 110
 Gly Phe Met Leu Ile Trp Asp Ser Ala Ser Gly Leu Lys Gln Asn Ala
 115 120 125
 Ile Pro Leu Asp Ser Gln Trp Val Leu Ser Cys Ala Ile Ser Pro Ser
 130 135 140
 Ser Thr Leu Val Ala Ser Ala Gly Leu Asn Asn Asn Cys Thr Ile Tyr
 145 150 155 160
 Arg Val Ser Lys Glu Asn Arg Val Ala Gln Asn Val Ala Ser Ile Phe
 165 170 175
 Lys Gly His Thr Cys Tyr Ile Ser Asp Ile Glu Phe Thr Asp Asn Ala
 180 185 190
 His Ile Leu Thr Ala Ser Gly Asp Met Thr Cys Ala Leu Trp Asp Ile

195	200	205
Pro Lys Ala Lys Arg Val	Arg Glu Tyr Ser Asp	His Leu Gly Asp Val
210	215	220
Leu Ala Leu Ala Ile Pro Glu Glu Pro Asn Leu Glu Asn Ser Ser Asn		
225	230	235 240
Thr Phe Ala Ser Cys Gly Ser Asp Gly Tyr Thr Tyr Ile Trp Asp Ser		
	245	250 255
Arg Ser Pro Ser Ala Val Gln Ser Phe Tyr Val Asn Asp Ser Asp Ile		
	260	265 270
Asn Ala Leu Arg Phe Phe Lys Asp Gly Met Ser Ile Val Ala Gly Ser		
	275	280 285
Asp Asn Gly Ala Ile Asn Met Tyr Asp Leu Arg Ser Asp Cys Ser Ile		
	290	295 300
Ala Thr Phe Ser Leu Phe Arg Gly Tyr Glu Glu Arg Thr Pro Thr Pro		
305	310	315 320
Thr Tyr Met Ala Ala Asn Met Glu Tyr Asn Thr Ala Gln Ser Pro Gln		
	325	330 335
Thr Leu Lys Ser Thr Ser Ser Ser Tyr Leu Asp Asn Gln Gly Ala Val		
	340	345 350
Ser Leu Asp Phe Ser Ala Ser Gly Arg Leu Met Tyr Ser Cys Tyr Thr		
	355	360 365
Asp Ile Gly Cys Val Val Trp Asp Val Leu Lys Gly Glu Ile Val Gly		
	370	375 380
Lys Leu Glu Gly His Gly Gly Arg Val Thr Gly Val Arg Ser Ser Pro		
385	390	395 400
Asp Gly Leu Ala Val Cys Thr Gly Ser Trp Asp Ser Thr Met Lys Ile		
	405	410 415
Trp Ser Pro Gly Tyr Gln		
	420	

<210> 16
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: amino acid
 sequence

<400> 16
 Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 17
 <211> 7

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 17
Gln Asn Leu Tyr Phe Gln Gly
1 5

<210> 18
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 18
Gln Phe Lys Leu Pro Val Ile Ala Phe Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 19
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 19
Gln Phe Lys Leu Pro Val Ile Ala Ser Gly Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 20
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: amino acid
sequence

<400> 20
Gln Phe Lys Leu Pro Val Ile Ala Pro Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 21

<211> 19
<212> PRT
<213> *Saccharomyces cerevisiae*

<220>
<223>

<400> 21
Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys
1 5 10 15

Lys Ser Ile

<210> 22
<211> 19
<212> PRT
<213> Human

<220>
<223>

<400> 22
Gln Tyr Glu Phe Asp Val Ile Leu Ser Pro Glu Leu Lys Val Gln Met
1 5 10 15

Lys Thr Ile

<210> 23
<211> 2535
<212> DNA
<213> *Candida albicans*

<400> 23
atggaacatc caccagcagc tctcagaaca ttttcaaccc aatcaacttc atcttttgaat 60
tcagtaagta ctgttttcgtc ttcaagaatt gtttctctg gcccagtcaa tataaacaat 120
ttcaataaac caagtactcc caaagaccat ttattctatc gatgtgaatc actaaaacga 180
aaactacaaa aaatccctgg catggaacca tttttgaacc aagctttcaa tcaggctgaa 240
caactcagtg aacaacaagc attggctttg gcacaggaaa gaagcaatgg aaatggacat 300
agtaatggca aacgtcatca atcattagac ggtgccatga atagactttc agttggttct 360
gatagtagtt cgatccaagg ttcattgaca cgaatggcca ccaatgcgtc aacgtcatct 420
ttaatcagtg gtatgcaaaa caacaacact ttatttacgt ttactgcagg ggttttacca 480
gctaataatta gtgtcgatcc tgctacccat ctttggaaat tgttccaaca agggggcccc 540
ttttgtgttc ttatcaatca tatccttctt gattcccaaa taccagttgt cagttctgat 600
gacttgagaa tttgcaaaaa atcagtatat gactttttaa ttgccgtcaa gacacaattg 660
aattttgatg acgagaatat gttcactata tccaatgttt tctccgacaa tgccaagat 720
ttaatcaaga ttattgatgt cathtaataaa ctacttgctg agtactcaga tgctagtga 780
ctgggtgggtg gcgatgaaga tgtaaatatg gatgttcaaa ttaccgatga aagatcaaaa 840
gttttccgag aaattatcga aacagaaaga aaatatgttc aagacttggg actaatgtgt 900
aaataccgtc aagatctaata tgaagccgaa aatttgtctt cagaacaaat tcacttggt 960
ttcccaaaatt taaatgagat tattgatttt caaagacgat tcctcaatgg gttagaatgt 1020
aacatcaatg tacttattag atatcaaaga attggatcag tatttattca tgcttctttg 1080
ggccctttca atgcttatga accttggact ataggacaat tgacggcgat tgatttgatc 1140
aacaagaag ctgctaattt gaaaaaatcg tcaagtctac ttgatcctgg gtttgaactt 1200
caatcgata tattaaagct gatccaaaga ttgtgtaaat acccactttt gttgaaagag 1260
ttaatcaaaa catcaccaga atattcaaaa caggaccccc atggcagctc gtcacgcaga 1320
tcattcaatg aattattggt ggctaaaact gcaatgaaag aattggcaaa tcaagtcaat 1380
gaggcgcaaa gacgagcaga aaatatcgaa catttggaaa aactaaaaga aagagtaggt 1440
aattggcgtg ggtttaattt ggatgctcaa ggagaactat tattccaagg acaagttggg 1500

gttaaagatg ctgaaaatga aaaggaatac gttgcttatac tttttgaaaa aatcgtattt 1560
 tttttcacag aaattgatga taccaaaaaa tctgataaac aggaaaagaa gagcaagttt 1620
 tcgacaagaa agagatcaac ttcatacaat cttagttcat cgactactaa tttgttgga 1680
 tcaataaaca attcccgaag ggataacaca ttgccattgg aattaaaggg aagagtttat 1740
 atatcgagga tttataacat ttccgcacca aacactcctg gctcaactct aatcatctca 1800
 tggtcaggta gaaaggaaag cggctcattc actttgagat atcgtagtga agaagccaga 1860
 aaccaatggg aaaagtgttt acgtgatttg aagactaatg aaatgaataa acaaattcat 1920
 aagaagttac gtgattccga cctgtcattt aatactgatg actctgccat atatgattac 1980
 acgggtatta gtacgtcacc agtcaatcaa tcaactcaac aacaatacta tgatcatcgg 2040
 ggctctcaca gttcccgcga tcaactcatg tcatccactt tgagtatgat gaagaataat 2100
 agagttaaag ctggtgattt gtagtagaata tcttcaactt caacaacatt agattctttc 2160
 agtaacaact tgaatgggtc accaaatacc actaatccat ctttgatgtc ttcagatgcc 2220
 accaaaacaa ttccaacatt tgacgttgca attaaattgc tttacaaatc gacagaattg 2280
 tcagagccat tgattgtcaa tgcacaaatt gagtataatg accttttaca gaaaattatc 2340
 tcccagatta tcacttcgaa cttggtggca gatgatgtca atattagtcg attgagatat 2400
 aaagacgacg aaggagactt tgtgaatttg aattcagatg atgattgggg gttagtgtt 2460
 gatattgtaa ccagtgaaga cttttaccaa acatcaagca atgaaaaacg actggtgaca 2520
 gtgtgggttt cttga 2535

<210> 24
 <211> 844
 <212> PRT
 <213> Candida albicans

<400> 24
 Met Glu His Pro Pro Ala Ala Leu Arg Thr Phe Ser Thr Gln Ser Thr
 1 5 10 15
 Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile Val Ser
 20 25 30
 Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr Pro Lys
 35 40 45
 Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu Gln Lys
 50 55 60
 Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln Ala Glu
 65 70 75 80
 Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg Ser Asn
 85 90 95
 Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp Gly Ala
 100 105 110
 Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln Gly Ser
 115 120 125
 Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile Ser Gly
 130 135 140
 Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val Leu Pro
 145 150 155 160
 Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu Phe Gln
 165 170 175
 Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser
 180 185 190

Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
 195 200 205
 Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp
 210 215 220
 Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp
 225 230 235 240
 Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr Ser
 245 250 255
 Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met Asp Val
 260 265 270
 Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile Glu Thr
 275 280 285
 Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr Arg Gln
 290 295 300
 Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His Leu Leu
 305 310 315 320
 Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe Leu Asn
 325 330 335
 Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg Ile Gly
 340 345 350
 Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr Glu Pro
 355 360 365
 Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys Glu Ala
 370 375 380
 Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe Glu Leu
 385 390 395 400
 Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr Pro Leu
 405 410 415
 Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys Gln Asp
 420 425 430
 Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu Val Ala
 435 440 445
 Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala Gln Arg
 450 455 460
 Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg Val Gly
 465 470 475 480
 Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu Phe His
 485 490 495
 Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr Val Ala
 500 505 510

Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp Asp Thr
 515 520 525
 Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr Arg Lys
 530 535 540
 Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu Leu Glu
 545 550 555 560
 Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys
 565 570 575
 Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr
 580 585 590
 Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly
 595 600 605
 Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu
 610 615 620
 Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln Ile His
 625 630 635 640
 Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp Ser Ala
 645 650 655
 Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln Ser Thr
 660 665 670
 Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His His
 675 680 685
 Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val Lys Ser
 690 695 700
 Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp Ser Phe
 705 710 715 720
 Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Met
 725 730 735
 Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys
 740 745 750
 Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala
 755 760 765
 Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln Ile Ile
 770 775 780
 Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu Arg Tyr
 785 790 795 800
 Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp Asp Trp
 805 810 815
 Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser
 820 825 830
 Ser Asn Glu Lys Arg Ser Val Thr Val Trp Val Ser

835

840

<210> 25
 <211> 22
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 25
 Lys Leu Pro Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser
 1 5 10 15

Ile Tyr Asp Phe Ile Leu
 20

<210> 26
 <211> 22
 <212> PRT
 <213> *Candida albicans*

<400> 26
 Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser
 1 5 10 15

Val Tyr Asp Phe Leu Ile
 20

<210> 27
 <211> 854
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 27
 Met Ala Ile Gln Thr Arg Phe Ala Ser Gly Thr Ser Leu Ser Asp Leu
 1 5 10 15

Lys Pro Lys Pro Ser Ala Thr Ser Ile Ser Ile Pro Met Gln Asn Val
 20 25 30

Met Asn Lys Pro Val Thr Glu Gln Asp Ser Leu Phe His Ile Cys Ala
 35 40 45

Asn Ile Arg Lys Arg Leu Glu Val Leu Pro Gln Leu Lys Pro Phe Leu
 50 55 60

Gln Leu Ala Tyr Gln Ser Ser Glu Val Leu Ser Glu Arg Gln Ser Leu
 65 70 75 80

Leu Leu Ser Gln Lys Gln His Gln Glu Leu Leu Lys Ser Asn Gly Ala
 85 90 95

Asn Arg Asp Ser Ser Asp Leu Ala Pro Thr Leu Arg Ser Ser Ile
 100 105 110

Ser Thr Ala Thr Ser Leu Met Ser Met Glu Gly Ile Ser Tyr Thr Asn
 115 120 125

Ser Asn Pro Ser Ala Thr Pro Asn Met Glu Asp Thr Leu Leu Thr Phe
 130 135 140

Ser Met Gly Ile Leu Pro Ile Thr Met Asp Cys Asp Pro Val Thr Gln
 145 150 155 160
 Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu Cys Ile Leu Phe Asn
 165 170 175
 Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile Ala Ser Asp Asp Leu
 180 185 190
 Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile Leu Gly Cys Lys Lys
 195 200 205
 His Phe Ala Phe Asn Asp Glu Glu Leu Phe Thr Ile Ser Asp Val Phe
 210 215 220
 Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu Glu Val Val Glu Thr
 225 230 235 240
 Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser Lys Ser Lys Thr Gln
 245 250 255
 Gln Ile Met Asn Ala Glu Asn Gln His Arg His Gln Pro Gln Gln Ser
 260 265 270
 Ser Lys Lys His Asn Glu Tyr Val Lys Ile Ile Lys Glu Phe Val Ala
 275 280 285
 Thr Glu Arg Lys Tyr Val His Asp Leu Glu Ile Leu Asp Lys Tyr Arg
 290 295 300
 Gln Gln Leu Leu Asp Ser Asn Leu Ile Thr Ser Glu Glu Leu Tyr Met
 305 310 315 320
 Leu Phe Pro Asn Leu Gly Asp Ala Ile Asp Phe Gln Arg Arg Phe Leu
 325 330 335
 Ile Ser Leu Glu Ile Asn Ala Leu Val Glu Pro Ser Lys Gln Arg Ile
 340 345 350
 Gly Ala Leu Phe Met His Ser Lys His Phe Phe Lys Leu Tyr Glu Pro
 355 360 365
 Trp Ser Ile Gly Gln Asn Ala Ala Ile Glu Phe Leu Ser Ser Thr Leu
 370 375 380
 His Lys Met Arg Val Asp Glu Ser Gln Arg Phe Ile Ile Asn Asn Lys
 385 390 395 400
 Leu Glu Leu Gln Ser Phe Leu Tyr Lys Pro Val Gln Arg Leu Cys Arg
 405 410 415
 Tyr Pro Leu Leu Val Lys Glu Leu Leu Ala Glu Ser Ser Asp Asp Asn
 420 425 430
 Asn Thr Lys Glu Leu Glu Ala Ala Leu Asp Ile Ser Lys Asn Ile Ala
 435 440 445
 Arg Ser Ile Asn Glu Asn Gln Arg Arg Thr Glu Asn His Gln Val Val
 450 455 460

Lys Lys Leu Tyr Gly Arg Val Val Asn Trp Lys Gly Tyr Arg Ile Ser
 465 470 475 480
 Lys Phe Gly Glu Leu Leu Tyr Phe Asp Lys Val Phe Ile Ser Thr Thr
 485 490 495
 Asn Ser Ser Ser Glu Pro Glu Arg Glu Phe Glu Val Tyr Leu Phe Glu
 500 505 510
 Lys Ile Ile Ile Leu Phe Ser Glu Val Val Thr Lys Lys Ser Ala Ser
 515 520 525
 Ser Leu Ile Leu Lys Lys Lys Ser Ser Thr Ser Ala Ser Ile Ser Ala
 530 535 540
 Ser Asn Ile Thr Asp Asn Asn Gly Ser Pro His His Ser Tyr His Lys
 545 550 555 560
 Arg His Ser Asn Ser Ser Ser Ser Asn Asn Ile His Leu Ser Ser Ser
 565 570 575
 Ser Ala Ala Ala Ile Ile His Ser Ser Thr Asn Ser Ser Asp Asn Asn
 580 585 590
 Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys Leu Ser Ala Asn Glu
 595 600 605
 Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile Met Asn Leu Asn Gln
 610 615 620
 Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile Thr Trp Glu Ser Ile
 625 630 635 640
 Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys Asn Glu Glu Thr Arg
 645 650 655
 Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile His Asp Leu Lys Asn
 660 665 670
 Glu Gln Phe Lys Ala Arg His His Ser Ser Thr Ser Thr Thr Ser Ser
 675 680 685
 Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr Thr Thr Met Asn Thr
 690 695 700
 Pro Asn His His Asn Ser Arg Gln Thr His Asp Ser Met Ala Ser Phe
 705 710 715 720
 Ser Ser Ser His Met Lys Arg Val Ser Asp Val Leu Pro Lys Arg Arg
 725 730 735
 Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys Ser Ile Ser Glu Asn
 740 745 750
 Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu Phe Arg Ile Ser Tyr
 755 760 765
 Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu Ile Phe Thr Leu Leu
 770 775 780
 Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile Met Ala Ile Asn Ser

[illegible]

```
<210> 28
<211> 837
<212> PRT
<213> Saccharomyces cerevisiae
```

<400> 28																
Ser	Gly	Thr	Ser	Leu	Ser	Asp	Leu	Lys	Pro	Lys	Pro	Ser	Ala	Thr	Ser	
1				5					10					15		
Ile	Ser	Ile	Pro	Met	Gln	Asn	Val	Met	Asn	Lys	Pro	Val	Thr	Glu	Gln	
			20					25					30			
Asp	Ser	Leu	Phe	His	Ile	Cys	Ala	Asn	Ile	Arg	Lys	Arg	Leu	Glu	Val	
		35					40					45				
Leu	Pro	Gln	Leu	Lys	Pro	Phe	Leu	Gln	Leu	Ala	Tyr	Gln	Ser	Ser	Glu	
	50					55					60					
Val	Leu	Ser	Glu	Arg	Gln	Ser	Leu	Leu	Leu	Ser	Gln	Lys	Gln	His	Gln	
65					70					75					80	
Glu	Leu	Leu	Lys	Ser	Asn	Gly	Ala	Asn	Arg	Asp	Ser	Ser	Asp	Leu	Ala	
				85					90					95		
Pro	Thr	Leu	Arg	Ser	Ser	Ser	Ile	Ser	Thr	Ala	Thr	Ser	Leu	Met	Ser	
			100					105					110			
Met	Glu	Gly	Ile	Ser	Tyr	Thr	Asn	Ser	Asn	Pro	Ser	Ala	Thr	Pro	Asn	
		115					120					125				
Met	Glu	Asp	Thr	Leu	Leu	Thr	Phe	Ser	Met	Gly	Ile	Leu	Pro	Ile	Thr	
	130					135					140					
Met	Asp	Cys	Asp	Pro	Val	Thr	Gln	Leu	Ser	Gln	Leu	Phe	Gln	Gln	Gly	
145					150					155					160	
Ala	Pro	Leu	Cys	Ile	Leu	Phe	Asn	Ser	Val	Lys	Pro	Gln	Phe	Lys	Leu	
				165					170					175		
Pro	Val	Ile	Ala	Ser	Asp	Asp	Leu	Lys	Val	Cys	Lys	Lys	Ser	Ile	Tyr	
			180					185					190			
Asp	Phe	Ile	Leu	Gly	Cys	Lys	Lys	His	Phe	Ala	Phe	Asn	Asp	Glu	Glu	
		195					200					205				
Leu	Phe	Thr	Ile	Ser	Asp	Val	Phe	Ala	Asn	Ser	Thr	Ser	Gln	Leu	Val	

210	215	220
Lys Val Leu Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile 225 230 235 240		
Phe Pro Ser Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln 245 250 255		
His Arg His Gln Pro Gln Gln Ser Ser Lys Lys His Asn Glu Tyr Val 260 265 270		
Lys Ile Ile Lys Glu Phe Val Ala Thr Glu Arg Lys Tyr Val His Asp 275 280 285		
Leu Glu Ile Leu Asp Lys Tyr Arg Gln Gln Leu Leu Asp Ser Asn Leu 290 295 300		
Ile Thr Ser Glu Glu Leu Tyr Met Leu Phe Pro Asn Leu Gly Asp Ala 305 310 315 320		
Ile Asp Phe Gln Arg Arg Phe Leu Ile Ser Leu Glu Ile Asn Ala Leu 325 330 335		
Val Glu Pro Ser Lys Gln Arg Ile Gly Ala Leu Phe Met His Ser Lys 340 345 350		
His Phe Phe Lys Leu Tyr Glu Pro Trp Ser Ile Gly Gln Asn Ala Ala 355 360 365		
Ile Glu Phe Leu Ser Ser Thr Leu His Lys Met Arg Val Asp Glu Ser 370 375 380		
Gln Arg Phe Ile Ile Asn Asn Lys Leu Glu Leu Gln Ser Phe Leu Tyr 385 390 395 400		
Lys Pro Val Gln Arg Leu Cys Arg Tyr Pro Leu Leu Val Lys Glu Leu 405 410 415		
Leu Ala Glu Ser Ser Asp Asp Asn Asn Thr Lys Glu Leu Glu Ala Ala 420 425 430		
Leu Asp Ile Ser Lys Asn Ile Ala Arg Ser Ile Asn Glu Asn Gln Arg 435 440 445		
Arg Thr Glu Asn His Gln Val Val Lys Lys Leu Tyr Gly Arg Val Val 450 455 460		
Asn Trp Lys Gly Tyr Arg Ile Ser Lys Phe Gly Glu Leu Leu Tyr Phe 465 470 475 480		
Asp Lys Val Phe Ile Ser Thr Thr Asn Ser Ser Ser Glu Pro Glu Arg 485 490 495		
Glu Phe Glu Val Tyr Leu Phe Glu Lys Ile Ile Ile Leu Phe Ser Glu 500 505 510		
Val Val Thr Lys Lys Ser Ala Ser Ser Leu Ile Leu Lys Lys Lys Ser 515 520 525		
Ser Thr Ser Ala Ser Ile Ser Ala Ser Asn Ile Thr Asp Asn Asn Gly 530 535 540		

Ser	Pro	His	His	Ser	Tyr	His	Lys	Arg	His	Ser	Asn	Ser	Ser	Ser	Ser	
545					550					555						560
Asn	Asn	Ile	His	Leu	Ser	Ser	Ser	Ser	Ala	Ala	Ala	Ile	Ile	His	Ser	
				565					570							575
Ser	Thr	Asn	Ser	Ser	Asp	Asn	Asn	Ser	Asn	Asn	Ser	Ser	Ser	Ser	Ser	
			580					585								590
Leu	Phe	Lys	Leu	Ser	Ala	Asn	Glu	Pro	Lys	Leu	Asp	Leu	Arg	Gly	Arg	
		595					600					605				
Ile	Met	Ile	Met	Asn	Leu	Asn	Gln	Ile	Ile	Pro	Gln	Asn	Asn	Arg	Ser	
	610					615					620					
Leu	Asn	Ile	Thr	Trp	Glu	Ser	Ile	Lys	Glu	Gln	Gly	Asn	Phe	Leu	Leu	
625					630					635						640
Lys	Phe	Lys	Asn	Glu	Glu	Thr	Arg	Asp	Asn	Trp	Ser	Ser	Cys	Leu	Gln	
				645					650					655		
Gln	Leu	Ile	His	Asp	Leu	Lys	Asn	Glu	Gln	Phe	Lys	Ala	Arg	His	His	
			660					665					670			
Ser	Ser	Thr	Ser	Thr	Thr	Ser	Ser	Thr	Ala	Lys	Ser	Ser	Ser	Met	Met	
		675					680					685				
Ser	Pro	Thr	Thr	Thr	Met	Asn	Thr	Pro	Asn	His	His	Asn	Ser	Arg	Gln	
	690					695					700					
Thr	His	Asp	Ser	Met	Ala	Ser	Phe	Ser	Ser	Ser	His	Met	Lys	Arg	Val	
705					710					715						720
Ser	Asp	Val	Leu	Pro	Lys	Arg	Arg	Thr	Thr	Ser	Ser	Ser	Phe	Glu	Ser	
				725					730					735		
Glu	Ile	Lys	Ser	Ile	Ser	Glu	Asn	Phe	Lys	Asn	Ser	Ile	Pro	Glu	Ser	
			740					745					750			
Ser	Ile	Leu	Phe	Arg	Ile	Ser	Tyr	Asn	Asn	Asn	Ser	Asn	Asn	Thr	Ser	
		755					760					765				
Ser	Ser	Glu	Ile	Phe	Thr	Leu	Leu	Val	Glu	Lys	Val	Trp	Asn	Phe	Asp	
	770					775					780					
Asp	Leu	Ile	Met	Ala	Ile	Asn	Ser	Lys	Ile	Ser	Asn	Thr	His	Asn	Asn	
785				790						795					800	
Asn	Ile	Ser	Pro	Ile	Thr	Lys	Ile	Lys	Tyr	Gln	Asp	Glu	Asp	Gly	Asp	
				805					810					815		
Phe	Val	Val	Leu	Gly	Ser	Asp	Glu	Asp	Trp	Asn	Val	Ala	Lys	Glu	Met	
			820				825						830			
Leu	Ala	Glu	Asn	Asn												
			835													

<210> 29

<211> 813

<212> PRT

<213> Candida albicans

<400> 29

Ser Thr Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg Ile
1 5 10 15

Val Ser Ser Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr
20 25 30

Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu Lys Arg Lys Leu
35 40 45

Gln Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln
50 55 60

Ala Glu Gln Leu Ser Glu Gln Gln Ala Leu Ala Leu Ala Gln Glu Arg
65 70 75 80

Ser Asn Gly Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp
85 90 95

Gly Ala Met Asn Arg Leu Ser Val Gly Ser Asp Ser Ser Ser Ile Gln
100 105 110

Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile
115 120 125

Ser Gly Met Pro Asn Asn Asn Thr Leu Phe Thr Phe Thr Ala Gly Val
130 135 140

Leu Pro Ala Asn Ile Ser Val Asp Pro Ala Thr His Leu Trp Lys Leu
145 150 155 160

Phe Gln Gln Gly Ala Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro
165 170 175

Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
180 185 190

Lys Ser Val Tyr Asp Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe
195 200 205

Asp Asp Glu Asn Met Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala
210 215 220

Gln Asp Leu Ile Lys Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu
225 230 235 240

Tyr Ser Asp Ala Ser Asp Ser Gly Gly Gly Asp Glu Asp Val Asn Met
245 250 255

Asp Val Gln Ile Thr Asp Glu Arg Ser Lys Val Phe Arg Glu Ile Ile
260 265 270

Glu Thr Glu Arg Lys Tyr Val Gln Asp Leu Glu Leu Met Cys Lys Tyr
275 280 285

Arg Gln Asp Leu Ile Glu Ala Glu Asn Leu Ser Ser Glu Gln Ile His
290 295 300

Leu Leu Phe Pro Asn Leu Asn Glu Ile Ile Asp Phe Gln Arg Arg Phe
 305 310 315 320
 Leu Asn Gly Leu Glu Cys Asn Ile Asn Val Pro Ile Arg Tyr Gln Arg
 325 330 335
 Ile Gly Ser Val Phe Ile His Ala Ser Leu Gly Pro Phe Asn Ala Tyr
 340 345 350
 Glu Pro Trp Thr Ile Gly Gln Leu Thr Ala Ile Asp Leu Ile Asn Lys
 355 360 365
 Glu Ala Ala Asn Leu Lys Lys Ser Ser Ser Leu Leu Asp Pro Gly Phe
 370 375 380
 Glu Leu Gln Ser Tyr Ile Leu Lys Pro Ile Gln Arg Leu Cys Lys Tyr
 385 390 395 400
 Pro Leu Leu Leu Lys Glu Leu Ile Lys Thr Ser Pro Glu Tyr Ser Lys
 405 410 415
 Gln Asp Pro His Gly Ser Ser Ser Ser Thr Ser Phe Asn Glu Leu Leu
 420 425 430
 Val Ala Lys Thr Ala Met Lys Glu Leu Ala Asn Gln Val Asn Glu Ala
 435 440 445
 Gln Arg Arg Ala Glu Asn Ile Glu His Leu Glu Lys Leu Lys Glu Arg
 450 455 460
 Val Gly Asn Trp Arg Gly Phe Asn Leu Asp Ala Gln Gly Glu Leu Leu
 465 470 475 480
 Phe His Gly Gln Val Gly Val Lys Asp Ala Glu Asn Glu Lys Glu Tyr
 485 490 495
 Val Ala Tyr Leu Phe Glu Lys Ile Val Phe Phe Phe Thr Glu Ile Asp
 500 505 510
 Asp Thr Lys Lys Ser Asp Lys Gln Glu Lys Lys Ser Lys Phe Ser Thr
 515 520 525
 Arg Lys Arg Ser Thr Ser Ser Asn Leu Ser Ser Ser Thr Thr Asn Leu
 530 535 540
 Leu Glu Ser Ile Asn Asn Ser Arg Lys Asp Asn Thr Leu Pro Leu Glu
 545 550 555 560
 Leu Lys Gly Arg Val Tyr Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro
 565 570 575
 Asn Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu
 580 585 590
 Ser Gly Ser Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln
 595 600 605
 Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln
 610 615 620
 Ile His Lys Lys Leu Arg Asp Ser Asp Ser Ser Phe Asn Thr Asp Asp

625 630 635 640
 Ser Ala Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro Val Asn Gln
 645 650 655
 Ser Thr Gln Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg
 660 665 670
 His His Ser Ser Ser Ser Thr Leu Ser Met Met Lys Asn Asn Arg Val
 675 680 685
 Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Ser Thr Thr Leu Asp
 690 695 700
 Ser Phe Ser Asn Asn Leu Asn Gly Ser Pro Asn Thr Thr Asn Pro Ser
 705 710 715 720
 Leu Met Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala
 725 730 735
 Ile Lys Leu Leu Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val
 740 745 750
 Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Gln Lys Ile Ile Ser Gln
 755 760 765
 Ile Ile Thr Ser Asn Leu Val Ala Asp Asp Val Asn Ile Ser Arg Leu
 770 775 780
 Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser Asp Asp
 785 790 795 800
 Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp
 805 810

<210> 30
 <211> 684
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 30
 Asp Pro Val Thr Gln Leu Ser Gln Leu Phe Gln Gln Gly Ala Pro Leu
 1 5 10 15
 Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro Val Ile
 20 25 30
 Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp Phe Ile
 35 40 45
 Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Leu Phe Thr
 50 55 60
 Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys Val Leu
 65 70 75 80
 Glu Val Val Glu Thr Leu Met Asn Ser Ser Pro Thr Ile Phe Pro Ser
 85 90 95
 Lys Ser Lys Thr Gln Gln Ile Met Asn Ala Glu Asn Gln His Arg His

100								105				110			
Gln	Pro	Gln	Gln	Ser	Ser	Lys	Lys	His	Asn	Glu	Tyr	Val	Lys	Ile	Ile
		115					120					125			
Lys	Glu	Phe	Val	Ala	Thr	Glu	Arg	Lys	Tyr	Val	His	Asp	Leu	Glu	Ile
	130					135					140				
Leu	Asp	Lys	Tyr	Arg	Gln	Gln	Leu	Leu	Asp	Ser	Asn	Leu	Ile	Thr	Ser
145					150					155					160
Glu	Glu	Leu	Tyr	Met	Leu	Phe	Pro	Asn	Leu	Gly	Asp	Ala	Ile	Asp	Phe
				165					170					175	
Gln	Arg	Arg	Phe	Leu	Ile	Ser	Leu	Glu	Ile	Asn	Ala	Leu	Val	Glu	Pro
			180					185					190		
Ser	Lys	Gln	Arg	Ile	Gly	Ala	Leu	Phe	Met	His	Ser	Lys	His	Phe	Phe
		195					200					205			
Lys	Leu	Tyr	Glu	Pro	Trp	Ser	Ile	Gly	Gln	Asn	Ala	Ala	Ile	Glu	Phe
	210					215					220				
Leu	Ser	Ser	Thr	Leu	His	Lys	Met	Arg	Val	Asp	Glu	Ser	Gln	Arg	Phe
225					230					235					240
Ile	Ile	Asn	Asn	Lys	Leu	Glu	Leu	Gln	Ser	Phe	Leu	Tyr	Lys	Pro	Val
				245					250					255	
Gln	Arg	Leu	Cys	Arg	Tyr	Pro	Leu	Leu	Val	Lys	Glu	Leu	Leu	Ala	Glu
			260					265					270		
Ser	Ser	Asp	Asp	Asn	Asn	Thr	Lys	Glu	Leu	Glu	Ala	Ala	Leu	Asp	Ile
		275					280					285			
Ser	Lys	Asn	Ile	Ala	Arg	Ser	Ile	Asn	Glu	Asn	Gln	Arg	Arg	Thr	Glu
	290					295					300				
Asn	His	Gln	Val	Val	Lys	Lys	Leu	Tyr	Gly	Arg	Val	Val	Asn	Trp	Lys
305					310					315					320
Gly	Tyr	Arg	Ile	Ser	Lys	Phe	Gly	Glu	Leu	Leu	Tyr	Phe	Asp	Lys	Val
				325					330					335	
Phe	Ile	Ser	Thr	Thr	Asn	Ser	Ser	Ser	Glu	Pro	Glu	Arg	Glu	Phe	Glu
			340					345					350		
Val	Tyr	Leu	Phe	Glu	Lys	Ile	Ile	Ile	Leu	Phe	Ser	Glu	Val	Val	Thr
		355					360					365			
Lys	Lys	Ser	Ala	Ser	Ser	Leu	Ile	Leu	Lys	Lys	Lys	Ser	Ser	Thr	Ser
		370				375					380				
Ala	Ser	Ile	Ser	Ala	Ser	Asn	Ile	Thr	Asp	Asn	Asn	Gly	Ser	Pro	His
385					390					395					400
His	Ser	Tyr	His	Lys	Arg	His	Ser	Asn	Ser	Ser	Ser	Ser	Asn	Asn	Ile
				405					410					415	
His	Leu	Ser	Ser	Ser	Ser	Ala	Ala	Ala	Ile	Ile	His	Ser	Ser	Thr	Asn
				420				425						430	

Ser Ser Asp Asn Asn Ser Asn Asn Ser Ser Ser Ser Ser Leu Phe Lys
 435 440 445
 Leu Ser Ala Asn Glu Pro Lys Leu Asp Leu Arg Gly Arg Ile Met Ile
 450 455 460
 Met Asn Leu Asn Gln Ile Ile Pro Gln Asn Asn Arg Ser Leu Asn Ile
 465 470 475 480
 Thr Trp Glu Ser Ile Lys Glu Gln Gly Asn Phe Leu Leu Lys Phe Lys
 485 490 495
 Asn Glu Glu Thr Arg Asp Asn Trp Ser Ser Cys Leu Gln Gln Leu Ile
 500 505 510
 His Asp Leu Lys Asn Glu Gln Phe Lys Ala Arg His His Ser Ser Thr
 515 520 525
 Ser Thr Thr Ser Ser Thr Ala Lys Ser Ser Ser Met Met Ser Pro Thr
 530 535 540
 Thr Thr Met Asn Thr Pro Asn His His Asn Ser Arg Gln Thr His Asp
 545 550 555 560
 Ser Met Ala Ser Phe Ser Ser Ser His Met Lys Arg Val Ser Asp Val
 565 570 575
 Leu Pro Lys Arg Arg Thr Thr Ser Ser Ser Phe Glu Ser Glu Ile Lys
 580 585 590
 Ser Ile Ser Glu Asn Phe Lys Asn Ser Ile Pro Glu Ser Ser Ile Leu
 595 600 605
 Phe Arg Ile Ser Tyr Asn Asn Asn Ser Asn Asn Thr Ser Ser Ser Glu
 610 615 620
 Ile Phe Thr Leu Leu Val Glu Lys Val Trp Asn Phe Asp Asp Leu Ile
 625 630 635 640
 Met Ala Ile Asn Ser Lys Ile Ser Asn Thr His Asn Asn Asn Ile Ser
 645 650 655
 Pro Ile Thr Lys Ile Lys Tyr Gln Asp Glu Asp Gly Asp Phe Val Val
 660 665 670
 Leu Gly Ser Asp Glu Asp Trp Asn Val Ala Lys Glu
 675 680

<210> 31
 <211> 742
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 31
 Asp Pro Val Thr Glu Ile Trp Leu Phe Cys Arg Leu Gly Tyr Pro Leu
 1 5 10 15
 Cys Ala Leu Phe Asn Cys Leu Pro Val Lys Gln Lys Leu Glu Val Asn
 20 25 30

Ser Ser Val Ser Leu Glu Asn Thr Asn Val Cys Lys Ala Ser Leu Tyr
 35 40 45
 Arg Phe Met Leu Met Cys Lys Asn Glu Leu Gly Leu Thr Asp Ala Ala
 50 55 60
 Leu Phe Ser Ile Ser Glu Ile Tyr Lys Pro Ser Thr Ala Pro Leu Val
 65 70 75 80
 Arg Ala Leu Gln Thr Ile Glu Leu Leu Leu Lys Lys Tyr Glu Val Ser
 85 90 95
 Asn Thr Thr Lys Ser Ser Ser Thr Pro Ser Pro Ser Thr Asp Asp Asn
 100 105 110
 Val Pro Thr Gly Thr Leu Asn Ser Leu Ile Ala Ser Gly Arg Arg Val
 115 120 125
 Thr Ala Glu Leu Tyr Glu Thr Glu Leu Lys Tyr Ile Gln Asp Leu Glu
 130 135 140
 Tyr Leu Ser Asn Tyr Met Val Ile Leu Gln Gln Lys Gln Ile Leu Ser
 145 150 155 160
 Gln Asp Thr Ile Leu Ser Ile Phe Thr Asn Leu Asn Glu Ile Leu Asp
 165 170 175
 Phe Gln Arg Arg Phe Leu Val Gly Leu Glu Met Asn Leu Ser Leu Pro
 180 185 190
 Val Glu Glu Gln Arg Leu Gly Ala Leu Phe Ile Ala Leu Glu Glu Gly
 195 200 205
 Phe Ser Val Tyr Gln Val Phe Cys Thr Asn Phe Pro Asn Ala Gln Gln
 210 215 220
 Leu Ile Ile Asp Asn Gln Asn Gln Leu Leu Lys Val Ala Asn Leu Leu
 225 230 235 240
 Glu Pro Ser Tyr Glu Leu Pro Ala Leu Leu Ile Lys Pro Ile Gln Arg
 245 250 255
 Ile Cys Lys Tyr Pro Leu Leu Leu Asn Gln Leu Leu Lys Gly Thr Pro
 260 265 270
 Ser Gly Tyr Gln Tyr Glu Glu Glu Leu Lys Gln Gly Met Ala Cys Val
 275 280 285
 Val Arg Val Ala Asn Gln Val Asn Glu Thr Arg Arg Ile His Glu Asn
 290 295 300
 Arg Asn Ala Ile Ile Glu Leu Glu Gln Arg Val Ile Asp Trp Lys Gly
 305 310 315 320
 Tyr Ser Leu Gln Tyr Phe Gly Gln Leu Leu Val Trp Asp Val Val Asn
 325 330 335
 Val Cys Lys Ala Asp Ile Glu Arg Glu Tyr His Val Tyr Leu Phe Glu
 340 345 350

Lys Ile Leu Leu Cys Cys Lys Glu Met Ser Thr Leu Lys Arg Gln Ala
 355 360 365
 Arg Ser Ile Ser Met Asn Lys Lys Thr Lys Arg Leu Asp Ser Leu Gln
 370 375 380
 Leu Lys Gly Arg Ile Leu Thr Ser Asn Ile Thr Thr Val Val Pro Asn
 385 390 395 400
 His His Met Gly Ser Tyr Ala Ile Gln Ile Phe Trp Arg Gly Asp Pro
 405 410 415
 Gln His Glu Ser Phe Ile Leu Lys Leu Arg Asn Glu Glu Ser His Lys
 420 425 430
 Leu Trp Met Ser Val Leu Asn Arg Leu Leu Trp Lys Asn Glu His Gly
 435 440 445
 Ser Pro Lys Asp Ile Arg Ser Ala Ala Ser Thr Pro Ala Asn Pro Val
 450 455 460
 Tyr Asn Arg Ser Ser Ser Gln Thr Ser Lys Gly Tyr Asn Ser Ser Asp
 465 470 475 480
 Tyr Asp Leu Leu Arg Thr His Ser Leu Asp Glu Asn Val Asn Ser Pro
 485 490 495
 Thr Ser Ile Ser Ser Pro Ser Ser Lys Ser Ser Pro Phe Thr Lys Thr
 500 505 510
 Thr Ser Lys Asp Thr Lys Ser Ala Thr Thr Thr Asp Glu Arg Pro Ser
 515 520 525
 Asp Phe Ile Arg Leu Asn Ser Glu Glu Ser Val Gly Thr Ser Ser Leu
 530 535 540
 Arg Thr Ser Gln Thr Thr Ser Thr Ile Val Ser Asn Asp Ser Ser Ser
 545 550 555 560
 Thr Ala Ser Ile Pro Ser Gln Ile Ser Arg Ile Ser Gln Val Asn Ser
 565 570 575
 Leu Leu Asn Asp Tyr Asn Tyr Asn Arg Gln Ser His Ile Thr Arg Val
 580 585 590
 Tyr Ser Gly Thr Asp Asp Gly Ser Ser Val Ser Ile Phe Glu Asp Thr
 595 600 605
 Ser Ser Ser Thr Lys Gln Lys Ile Phe Asp Gln Pro Thr Thr Asn Asp
 610 615 620
 Cys Asp Val Met Arg Pro Arg Gln Tyr Ser Tyr Ser Ala Gly Met Lys
 625 630 635 640
 Ser Asp Gly Ser Leu Leu Pro Ser Thr Lys His Thr Ser Leu Ser Ser
 645 650 655
 Ser Ser Thr Ser Thr Ser Leu Ser Val Arg Asn Thr Thr Asn Val Lys
 660 665 670
 Ile Arg Leu Arg Leu His Glu Val Ser Leu Val Leu Val Val Ala His

675 680 685

Asp Ile Thr Phe Asp Glu Leu Leu Ala Lys Val Glu His Lys Ile Lys
690 695 700

Leu Cys Gly Ile Leu Lys Gln Ala Val Pro Phe Arg Val Arg Leu Lys
705 710 715 720

Tyr Val Asp Glu Asp Gly Asp Phe Ile Thr Ile Thr Ser Asp Glu Asp
725 730 735

Val Leu Met Ala Phe Glu
740

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> misc_feature
<222> (12)
<223> n is a or c or g or t

<400> 32
aartayrtkc angayttrga 20

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> misc_feature
<222> (13)
<223> n is a or c or g or t

<400> 33
ratttttytcr aanarrta 18

<210> 34
<211> 76
<212> PRT
<213> Candida albicans

<400> 34
Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
1 5 10 15

Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
20 25 30

Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met

35 40 45
 Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
 50 55 60
 Ile Ile Asp Val Ile Asn Lys Leu Leu Ala Glu Tyr
 65 70 75
 <210> 35 <211> 19 <212> PRT <213> Candida albicans <400> 35
 Asp Ser Gln Ile Pro Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys
 1 5 10 15
 Lys Ser Val

 <210> 36
 <211> 73
 <212> PRT
 <213> Candida albicans

 <400> 36
 Pro Phe Cys Val Leu Ile Asn His Ile Leu Pro Asp Ser Gln Ile Pro
 1 5 10 15
 Val Val Ser Ser Asp Asp Leu Arg Ile Cys Lys Lys Ser Val Tyr Asp
 20 25 30
 Phe Leu Ile Ala Val Lys Thr Gln Leu Asn Phe Asp Asp Glu Asn Met
 35 40 45
 Phe Thr Ile Ser Asn Val Phe Ser Asp Asn Ala Gln Asp Leu Ile Lys
 50 55 60
 Ile Ile Asp Val Ile Asn Lys Leu Leu
 65 70
 <210> 37
 <211> 73
 <212> PRT
 <213> Saccharomyces cerevisiae

 <400> 37
 Pro Leu Cys Ile Leu Phe Asn Ser Val Lys Pro Gln Phe Lys Leu Pro
 1 5 10 15
 Val Ile Ala Ser Asp Asp Leu Lys Val Cys Lys Lys Ser Ile Tyr Asp
 20 25 30
 Phe Ile Leu Gly Cys Lys Lys His Phe Ala Phe Asn Asp Glu Glu Leu
 35 40 45
 Phe Thr Ile Ser Asp Val Phe Ala Asn Ser Thr Ser Gln Leu Val Lys
 50 55 60
 Val Leu Glu Val Val Glu Thr Leu Met
 65 70